Raw Sequence Listing Error Summary

| ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/537,710A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length

Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ____ Skipped Sequences
(OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences
(NEW RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.
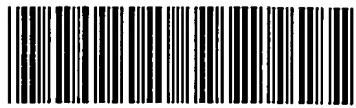
1600

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          RAW SEQUENCE LISTING                    DATE: 06/25/2002
          PATENT APPLICATION:  US/09/537,710A     TIME: 10:02:44

          Input Set : A:\PTO.VSK.txt
          Output Set: N:\CRF3\06252002\I537710A.raw
```

Handwritten annotations: "pp. 1,3-5, 8, 10, 12, 14-19, 21"; "Does Not Comply Corrected Diskette Needed"

```
   3 <110> APPLICANT: Dahlqvist, Andres
   4         Stahl, Ulf
   5         Lenman, Marit
   6         Banas, Antoni
   7         Ronne, Hans
   9 <120> TITLE OF INVENTION: A new class of enzymes in the biosynthetic pathway for the
production
  10         of
  11         triacylglycerol and recombinant DNA molecules encoding these enzymes
  13 <130> FILE REFERENCE: BASFnae337799PCT1-15
  15 <140> CURRENT APPLICATION NUMBER: US 09/537,710A
  17 <141> CURRENT FILING DATE: 2000-03-30
  19 <150> PRIOR APPLICATION NUMBER: EP 99106656.4
  20 <151> PRIOR FILING DATE: 1999-04-01
  22 <160> NUMBER OF SEQ ID NOS: 31
  24 <170> SOFTWARE: WordPerfect version 6.1
```

ERRORED SEQUENCES

Handwritten annotation: "invalid - This appears directly after Seq. 15"; "16 ← re-number this and subsequent sequences"

```
E--> 1228 <210> SEQ ID NO: (1a) 16
     1229 <211> LENGTH: 661
     1230 <212> TYPE: PRT
     1231 <213> ORGANISM: Saccharomyces cerevisiae
     1233 <400> SEQUENCE: (1a) 16
     1235 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
     1236  1               5                  10                  15
     1238 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
     1239             20                  25                  30
     1241 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
     1242         35                  40                  45
     1244 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
     1245     50                  55                  60
     1247 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
     1248 65                  70                  75                  80
     1250 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
     1251             85                  90                  95
     1253 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
     1254             100                 105                 110
     1256 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
     1257             115                 120                 125
     1259 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
     1260     130                 135                 140
     1262 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
```

Handwritten annotations: "Per 1.821 of Sequence Rules, "The sequence identifiers shall begin with 1 and increase sequentially by integers—""; "Please Note"

RAW SEQUENCE LISTING   DATE: 06/25/2002
PATENT APPLICATION: US/09/537,710A   TIME: 10:02:45

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\06252002\I537710A.raw

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1263 145              150              155              160
1265 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
1266          165              170              175
1268 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
1269          180              185              190
1271 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
1272          195              200              205
1274 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
1275     210              215              220
1277 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
1278 225              230              235              240
1280 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
1281          245              250              255
1283 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
1284          260              265              270
1286 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
1287          275              280              285
1289 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
1290     290              295              300
1292 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
1293 305              310              315              320
1295 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
1296          325              330              335
1298 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
1299          340              345              350
1301 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
1302          355              360              365
1304 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
1305     370              375              380
1307 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
1308 385              390              395              400
1310 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
1311              405              410              415
1313 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
1314          420              425              430
1316 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
1317          435              440              445
1319 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
1320     450              455              460
1322 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
1323 465              470              475              480
1325 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
1326          485              490              495
1328 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
1329          500              505              510
1331 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
1332          515              520              525
1334 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
1335     530              535              540
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●   ●

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1337 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
1338 545                 550                 555                 560
1340 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
1341                 565                 570                 575
1343 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
1344                 580                 585                 590
1346 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
1347                 595                 600                 605
1349 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
1350         610                 615                 620
1352 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
1353 625                 630                 635                 640
1355 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
1356                 645                 650                 655
1358 Met Pro Phe Pro Met
1359                 660
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E--> 1362 <210> SEQ ID NO: (2a) 17
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1363 <211> LENGTH: 387
1364 <212> TYPE: PRT
1365 <213> ORGANISM: Arabidopsis thaliana
1367 <400> SEQUENCE: (2a) 17
1369 Val Gly Ser Asn Val Tyr Pro Leu Ile Leu Val Pro Gly Asn Gly Gly
1370  1               5               10                  15
1372 Asn Gln Leu Glu Val Arg Leu Asp Arg Glu Tyr Lys Pro Ser Ser Val
1373                 20              25                  30
1375 Trp Cys Ser Ser Trp Leu Tyr Pro Ile His Lys Lys Ser Gly Gly Trp
1376             35              40              45
1378 Phe Arg Leu Trp Phe Asp Ala Ala Val Leu Leu Ser Pro Phe Thr Arg
1379         50              55              60
1381 Cys Phe Ser Asp Arg Met Met Leu Tyr Tyr Asp Pro Asp Leu Asp Asp
1382 65              70              75              80
1384 Tyr Gln Asn Ala Pro Gly Val Gln Thr Arg Val Pro His Phe Gly Ser
1385                 85              90              95
1387 Thr Lys Ser Leu Leu Tyr Leu Asp Pro Arg Leu Arg Asp Ala Thr Ser
1388             100             105             110
1390 Tyr Met Glu His Leu Val Lys Ala Leu Glu Lys Lys Cys Gly Tyr Val
1391         115             120             125
1393 Asn Asp Gln Thr Ile Leu Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu
1394         130             135             140
1396 Ala Ala Ser Gly His Pro Ser Arg Val Ala Ser Gln Phe Leu Gln Asp
1397 145             150             155             160
1399 Leu Lys Gln Leu Val Glu Lys Thr Ser Ser Glu Asn Glu Gly Lys Pro
1400             165             170             175
1402 Val Ile Leu Leu Ser His Ser Leu Gly Gly Leu Phe Val Leu His Phe
1403             180             185             190
1405 Leu Asn Arg Thr Thr Pro Ser Trp Arg Arg Lys Tyr Ile Lys His Phe
1406             195             200             205
1408 Val Ala Leu Ala Ala Pro Trp Gly Gly Thr Ile Ser Gln Met Lys Thr
1409         210             215             220
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1411 Phe Ala Ser Gly Asn Thr Leu Gly Val Pro Leu Val Asn Pro Leu Leu
1412 225             230             235         240
1414 Val Arg Arg His Gln Arg Thr Ser Glu Ser Asn Gln Trp Leu Leu Pro
1415             245             250             255
1417 Ser Thr Lys Val Phe His Asp Arg Thr Lys Pro Leu Val Val Thr Pro
1418             260             265             270
1420 Gln Val Asn Tyr Thr Ala Tyr Glu Met Asp Arg Phe Phe Ala Asp Ile
1421             275             280             285
1423 Gly Phe Ser Gln Gly Val Val Pro Tyr Lys Thr Arg Val Leu Pro Leu
1424     290             295             300
1426 Thr Glu Glu Leu Met Thr Pro Gly Val Pro Val Thr Cys Ile Tyr Gly
1427 305             310             315             320
1429 Arg Gly Val Asp Thr Pro Glu Val Leu Met Tyr Gly Lys Gly Gly Phe
1430             325             330             335
1432 Asp Lys Gln Pro Glu Ile Lys Tyr Gly Asp Gly Asp Gly Thr Val Asn
1433             340             345             350
1435 Leu Ala Ser Leu Ala Ala Leu Lys Val Asp Ser Leu Asn Thr Val Glu
1436             355             360             365
1438 Ile Asp Gly Val Ser His Thr Ser Ile Leu Lys Asp Glu Ile Ala Leu
1439     370             375             380
1441 Lys Glu Ile
1442 385
E--> 1445 <210> SEQ ID NO: ⟨3a⟩ 18
1446 <211> LENGTH: 389
1447 <212> TYPE: PRT
1448 <213> ORGANISM: Arabidopsis thaliana
1450 <400> SEQUENCE: 3a 18
1452 Leu Lys Lys Glu Gly Leu Lys Ala Lys His Pro Val Val Phe Ile Pro
1453   1             5             10             15
1455 Gly Ile Val Thr Gly Gly Leu Glu Leu Trp Glu Gly Lys Gln Cys Ala
1456             20             25             30
1458 Asp Gly Leu Phe Arg Lys Arg Leu Trp Gly Gly Thr Phe Leu Cys Trp
1459             35             40             45
1461 Val Glu His Met Ser Leu Asp Asn Glu Thr Gly Leu Asp Pro Ala Gly
1462     50             55             60
1464 Ile Arg Val Arg Ala Val Ser Gly Leu Val Ala Ala Asp Tyr Phe Ala
1465  65             70             75             80
1467 Pro Gly Tyr Phe Val Trp Ala Val Leu Ile Ala Asn Leu Ala His Ile
1468             85             90             95
1470 Gly Tyr Glu Glu Lys Asn Met Tyr Met Ala Ala Tyr Asp Trp Arg Leu
1471             100             105             110
1473 Ser Phe Gln Asn Thr Glu Arg Asp Gln Thr Leu Ser Arg Met Lys Ser
1474             115             120             125
1476 Asn Ile Glu Leu Met Val Ser Thr Asn Gly Gly Lys Lys Ala Val Ile
1477     130             135             140
1479 Val Pro His Ser Met Gly Val Leu Tyr Phe Leu His Phe Met Lys Trp
1480 145             150             155             160
1482 Val Glu Ala Pro Ala Pro Leu Gly Gly Gly Gly Pro Asp Trp Cys
1483             165             170             175
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1485 Ala Lys Tyr Ile Lys Ala Val Met Asn Ile Gly Gly Pro Phe Leu Gly
1486             180             185             190
1488 Val Pro Lys Ala Val Ala Gly Leu Phe Ser Ala Glu Ala Lys Asp Met .
1489             195             200             205
1491 Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu Pro Lys Gly
1492     210             215             220
1494 Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu Leu Pro Asn
1495 225             230             235             240
1497 Ala Pro Glu Met Glu Ile Tyr Ser Leu Tyr Gly Val Gly Ile Pro Thr
1498     .           245             250             255
1500 Glu Arg Ala Tyr Val Tyr Lys Leu Asn Gln Ser Pro Asp Ser Cys Ile
1501             260             265             270
1503 Pro Phe Gln Ile Phe Thr Ser Ala His Glu Glu Asp Glu Asp Ser Cys
1504             275             280             285
1506 Leu Lys Ala Gly Val Tyr Asn Val Asp Gly Asp Glu Thr Val Pro Val
1507         290             295             300
1509 Leu Ser Ala Gly Tyr Met Cys Ala Lys Ala Trp Arg Gly Lys Thr Arg
1510 305             310             315             320
1512 Phe Asn Pro Ser Gly Ile Lys Thr Tyr Ile Arg Glu Tyr Asn His Ser
1513             325             330             335
1515 Pro Pro Ala Asn Leu Leu Glu Gly Arg Gly Thr Gln Ser Gly Ala His
1516             340             345             350
1518 Val Asp Ile Met Gly Asn Phe Ala Leu Ile Glu Asp Ile Met Arg Val
1519         355             360             365
1521 Ala Ala Gly Gly Asn Gly Ser Asp Ile Gly His Asp Gln Val His Ser
1522     370             375             380
1524 Gly Ile Phe Glu Trp
1525 385
```

E--> 1528 <210> SEQ ID NO: (4a) 19
1529 <211> LENGTH: 1986
1530 <212> TYPE: DNA
1531 <213> ORGANISM: Saccharomyces cerevisiae
1533 <220> FEATURE:
1534 <221> NAME/KEY: CDS
1535 <222> LOCATION: (1)..(1983)
1537 <400> SEQUENCE: (4a) 19

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1539 atg ggc aca ctg ttt cga aga aat gtc cag aac caa aag agt gat tct   48
1540 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
1541   1               5                  10                  15
1543 gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga   96
1544 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
1545             20                  25                  30
1547 aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt  144
1548 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
1549             35                  40                  45
1551 att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg  192
1552 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
1553         50                  55                  60
1555 aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg  240
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1556 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
1557  65              70              75              80
1559 att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt    288
1560 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
1561              85              90              95
1563 ggc gct tat cat gtt cat aat agc gat agc gac ttg ttt gac aac ttt    336
1564 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
1565              100             105             110
1567 gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt    384
1568 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
1569              115             120             125
1571 ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac    432
1572 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
1573         130             135             140
1575 tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt    480
1576 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
1577 145             150             155             160
1579 aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta    528
1580 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
1581              165             170             175
1583 atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att    576
1584 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
1585              180             185             190
1587 gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg    624
1588 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
1589              195             200             205
1591 gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg    672
1592 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
1593         210             215             220
1595 ttg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac    720
1596 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
1597 225             230             235             240
1599 ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc    768
1600 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
1601              245             250             255
1603 gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att    816
1604 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
1605              260             265             270
1607 ggc tat gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt    864
1608 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
1609              275             280             285
1611 gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag    912
1612 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
1613         290             295             300
1615 gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aaa gtt tgt tta    960
1616 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
1617 305             310             315             320
1619 att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg   1008
1620 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
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1621                325                330                335
1623 gtc gag gct gaa ggc cct ctt tac ggt aat ggt ggt cgt ggc tgg gtt   1056
1624 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
1625                340                345                350
1627 aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc   1104
1628 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
1629                355                360                365
1631 gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc   1152
1632 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
1633      370                375                380
1635 att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca   1200
1636 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
1637 385                390                395                400
1639 aga att gag aga gta aaa atg tta caa acg tgg ggt ggt ata cca tca   1248
1640 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
1641                405                410                415
1643 atg cta cca aag gga gaa gag gtc att tgg ggg gat atg aag tca tct   1296
1644 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
1645                420                425                430
1647 tca gag gat gca ttg aat aac aac act gac aca tac ggc aat ttc att   1344
1648 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
1649                435                440                445
1651 cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg   1392
1652 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
1653      450                455                460
1655 aaa gac gcc att aac atg aca tta tcg ata tca cct gaa tgg ctc caa   1440
1656 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
1657 465                470                475                480
1659 aga aga gta cat gag cag tac tcg ttc ggc tat tcc aag aat gaa gaa   1488
1660 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
1661                485                490                495
1663 gag tta aga aaa aat gag cta cac cac aag cac tgg tcg aat cca atg   1536
1664 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
1665                500                505                510
1667 gaa gta cca ctt cca gaa gct ccc cac atg aaa atc tat tgt ata tac   1584
1668 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
1669      515                520                525
1671 ggg gtg aac aac cca act gaa agg gca tat gta tat aag gaa gag gat   1632
1672 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
1673      530                535                540
1675 gac tcc tct gct ctg aat ttg acc atc gac tac gaa agc aag caa cct   1680
1676 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
1677 545                550                555                560
1679 gta ttc ctc acc gag ggg gac gga acc gtt ccg ctc gtg gcg cat tca   1728
1680 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
1681                565                570                575
1683 atg tgt cac aaa tgg gcc cag ggt gct tca ccg tac aac cct gcc gga   1776
1684 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
1685                580                585                590
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1687 att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttt gat   1824
1688 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
1689         595                 600                 605
1691 ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc   1872
1692 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
1693         610                 615                 620
1695 gcg gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat   1920
1696 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
1697 625                 630                 635                 640
1699 ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag   1968
1700 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
1701                 645                 650                 655
1703 atg ccc ttc cca atg taa                                           1986
1704 Met Pro Phe Pro Met
1705                 660
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E--> 1708 <210> SEQ ID NO: (5a) 20
1709 <211> LENGTH: 661
1710 <212> TYPE: PRT
1711 <213> ORGANISM: Saccharomyces cerevisiae
1713 <400> SEQUENCE: (5a) 20

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1718 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
1719                 20                  25                  30
1721 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
1722         35                  40                  45
1724 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
1725         50                  55                  60
1727 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
1728 65                  70                  75                  80
1730 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
1731                 85                  90                  95
1733 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
1734                 100                 105                 110
1736 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
1737                 115                 120                 125
1739 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
1740         130                 135                 140
1742 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
1743 145                 150                 155                 160
1745 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
1746                 165                 170                 175
1748 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
1749                 180                 185                 190
1751 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
1752                 195                 200                 205
1754 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
1755         210                 215                 220
1757 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
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1758 225                   230               235                   240
1760 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
1761               245               250               255
1763 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
1764               260               265               270
1766 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
1767           275               280               285
1769 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
1770       290               295               300
1772 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
1773 305               310                . 315                   320
1775 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
1776               325               330               335
1778 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
1779           340               345               350
1781 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
1782           355               360               365
1784 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
1785       370               375               380
1787 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
1788 385               390               395                   400
1790 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
1791           405               410               415
1793 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
1794           420               425               430
1796 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
1797           435               440               445
1799 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
1800       450               455               460
1802 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
1803 465               470               475                   480
1805 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
1806               485               490               495
1808 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
1809           500               505               510
1811 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
1812           515               520               525
1814 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
1815       530               535               540
1817 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
1818 545               550               555                   560
1820 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
1821               565               570               575
1823 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
1824           580               585               590
1826 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
1827           595               600               605
1829 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
1830           610               615               620
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     1832 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
     1833 625                 630                 635                 640
     1835 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
     1836                 645                 650                 655
     1838 Met Pro Phe Pro Met
     1839                 660
E--> 1841 <210> SEQ ID NO: (1b) 21
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     1843 <212> TYPE: DNA
     1844 <213> ORGANISM: Saccharomyces cerevisiae
     1846 <220> FEATURE:
     1847 <221> NAME/KEY: CDS
     1848 <222> LOCATION: (1)..(1983)
     1850 <400> SEQUENCE: (1b) 21
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     1853 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
     1854   1               5                  10                  15
     1856 gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga    96
     1857 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
     1858               20                  25                  30
     1860 aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt   144
     1861 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
     1862           35                  40                  45
     1864 att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg   192
     1865 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
     1866       50                  55                  60
     1868 aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg   240
     1869 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
     1870   65                  70                  75                  80
     1872 att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt   288
     1873 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
     1874                   85                  90                  95
     1876 ggc gct tat cat gtt cat aat agc gat agc gac ttg ttt gac aac ttt   336
     1877 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
     1878              100                 105                 110
     1880 gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt   384
     1881 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
     1882          115                 120                 125
     1884 ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac   432
     1885 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
     1886      130                 135                 140
     1888 tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt   480
     1889 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
     1890 145                 150                 155                 160
     1892 aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta   528
     1893 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
     1894                 165                 170                 175
     1896 atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att   576
     1897 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
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1898            180                 185                 190
1900 gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg    624
1901 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
1902        195                 200                 205
1904 gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg    672
1905 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
1906        210                 215                 220
1908 ttg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac    720
1909 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
1910 225                 230                 235                 240
1912 ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc    768
1913 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
1914                245                 250                 255
1916 gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att    816
1917 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
1918                260                 265                 270
1920 ggc tat gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt    864
1921 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
1922                275                 280                 285
1924 gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag    912
1925 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
1926        290                 295                 300
1928 gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aaa gtt tgt tta    960
1929 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
1930 305                 310                 315                 320
1932 att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg    1008
1933 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
1934                325                 330                 335
1936 gtc gag gct gaa ggc cct ctt tac ggt aat ggt ggt cgt ggc tgg gtt    1056
1937 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
1938                340                 345                 350
1940 aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc    1104
1941 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
1942                355                 360                 365
1944 gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc    1152
1945 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
1946        370                 375                 380
1948 att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca    1200
1949 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
1950 385                 390                 395                 400
1952 aga att gag aga gta aaa atg tta caa acg tgg ggt ggt ata cca tca    1248
1953 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
1954                405                 410                 415
1956 atg cta cca aag gga gaa gag gtc att tgg ggg gat atg aag tca tct    1296
1957 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
1958        420                 425                 430
1960 tca gag gat gca ttg aat aac aac act gac aca tac ggc aat ttc att    1344
1961 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
1962        435                 440                 445
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1964 cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg   1392
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1966     450             455             460
1968 aaa gac gcc att aac atg aca tta tcg ata tca cct gaa tgg ctc caa   1440
1969 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
1970 465             470             475             480
1972 aga aga gta cat gag cag tac tcg ttc ggc tat tcc aag aat gaa gaa   1488
1973 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
1974             485             490             495
1976 gag tta aga aaa aat gag cta cac cac aag cac tgg tcg aat cca atg   1536
1977 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
1978         500             505             510
1980 gaa gta cca ctt cca gaa gct ccc cac atg aaa atc tat tgt ata tac   1584
1981 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
1982     515             520             525
1984 ggg gtg aac aac cca act gaa agg gca tat gta tat aag gaa gag gat   1632
1985 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
1986     530             535             540
1988 gac tcc tct gct ctg aat ttg acc atc gac tac gaa agc aag caa cct   1680
1989 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
1990 545             550             555             560
1992 gta ttc ctc acc gag ggg gac gga acc gtt ccg ctc gtg gcg cat tca   1728
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1994             565             570             575
1996 atg tgt cac aaa tgg gcc cag ggt gct tca ccg tac aac cct gcc gga   1776
1997 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
1998         580             585             590
2000 att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttt gat   1824
2001 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
2002         595             600             605
2004 ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc   1872
2005 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
2006     610             615             620
2008 gcg gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat   1920
2009 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
2010 625             630             635             640
2012 ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag   1968
2013 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
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2017 Met Pro Phe Pro Met
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2029   1   5   10   15

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2032             20               25              30
2034 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
2035         35              40               45
2037 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
2038     50              55              60
2040 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
2041 65              70              75              80
2043 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
2044             85              90              95
2046 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
2047         100             105             110
2049 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
2050         115             120             125
2052 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
2053     130             135             140
2055 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
2056 145             150             155             160
2058 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
2059             165             170             175
2061 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
2062         180             185             190
2064 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
2065         195             200             205
2067 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
2068     210             215             220
2070 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
2071 225             230             235             240
2073 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
2074             245             250             255
2076 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
2077         260             265             270
2079 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
2080         275             280             285
2082 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
2083     290             295             300
2085 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
2086 305             310             315             320
2088 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
2089             325             330             335
2091 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
2092         340             345             350
2094 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
2095         355             360             365
2097 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
2098     370             375             380
2100 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
2101 385             390             395             400
2103 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
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2104                   405                 410                 415
2106 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
2107           420                 425                 430
2109 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
2110           435                 440                 445
2112 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
2113      450                 455                 460
2115 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
2116 465                 470                 475                 480
2118 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
2119           485                 490                 495
2121 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
2122           500                 505                 510
2124 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
2125           515                 520                 525
2127 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
2128      530                 535                 540
2130 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
2131 545                 550                 555                 560
2133 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
2134           565                 570                 575
2136 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
2137           580                 585                 590
2139 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
2140           595                 600                 605
2142 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
2143      610                 615                 620
2145 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
2146 625                 630                 635                 640
2148 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
2149           645                 650                 655
2151 Met Pro Phe Pro Met
2152           660
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2159 <212> TYPE: DNA
2160 <213> ORGANISM: Schizosaccharomyces pombe
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2166 acacaatctg tttcaaataa atcaagaaaa tctaaatttg gaaaaagatt gaattttata 180
2167 ttgggcgcta ttttgggaat atgcggtgct ttttttttcg ctgttggaga cgacaatgct 240
2168 gttttcgacc ctgctacgtt agataaattt gggaatatgc taggctcttc agacttgttt 300
2169 gatgacatta aaggatattt atcttataat gtgtttaagg atgcaccttt tactacggac 360
2170 aagccttcgc agtctcctag cggaaatgaa gttcaagttg tcttgatat gtacaatgag 420
2171 ggatatcgaa gtgaccatcc tgttattatg gttcctggtg ttatcagctc aggattagaa 480
2172 agttggtcgt ttaataattg ctcgattcct tactttagga acgtctttg gggtagctgg 540
2173 tctatgctga aggcaatgtt ccttgacaag caatgctggc ttgaacattt aatgcttgat 600
2174 aaaaaaccg gcttggatcc gaagggaatt aagctgcgag cagctcaggg gtttgaagca 660
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RAW SEQUENCE LISTING   DATE: 06/25/2002
PATENT APPLICATION: US/09/537,710A   TIME: 10:02:45

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Output Set: **N:\CRF3\06252002\I537710A.raw**

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2178 attgtacata agaaaaaggt agtgttgatt tctcactcca tgggttcaca ggttacgtac 900
2179 tatttttta agtgggttga agctgagggc tacggaaatg gtggaccgac ttgggttaat 960
2180 gatcatattg aagcatttat aaatgtgagt ctcgatggtt gtttgactac gtttctaact 1020
2181 tttgaataga tatcgggatc tttgattgga gcacccaaaa cagtggcagc gcttttatcg 1080
2182 ggtgaaatga aagatacagg tattgtaatt acattaaaca tgttaatatt taattttgc 1140
2183 taaccgtttt aagctcaatt gaatcagttt tcggtctatg ggtaagcaat aaattgttga 1200
2184 gatttgttac taatttactg tttagtttgg aaaaatttt ttcccgttct gaggtatatt 1260
2185 caaaaataca aatgtgctct acttttcta actttaata gagagccatg atggttcgca 1320
2186 ctatgggagg agttagttct atgcttccta aaggaggcga tgttgtatgg ggaaatgcca 1380
2187 gttgggtaag aaatatgtgc tgttaatttt ttattaatat ttaggctcca gatgatctta 1440
2188 atcaaacaaa tttttccaat ggtgcaatta ttcgatatag agaagacatt gataaggacc 1500
2189 acgatgaatt tgacatagat gatgcattac aatttttaaa aaatgttaca gatgacgatt 1560
2190 ttaaagtcat gctagcgaaa aattattccc acggtcttgc ttggactgaa aaagaagtgt 1620
2191 taaaaaataa cgaaatgccg tctaaatgga taaatccgct agaagtaaga acattaaagt 1680
2192 tactaaatta tactaaccca aatagactag tcttccttat gctcctgata tgaaaattta 1740
2193 ttgcgttcac ggggtcggaa aaccaactga gagaggttat tattatacta ataatcctga 1800
2194 ggggcaacct gtcattgatt cctcggttaa tgatggaaca aaagttgaaa atgtgagaga 1860
2195 atttatgttt caaacattct attaactgtt ttattagggt attgttatgg atgatggtga 1920
2196 tggaacttta ccaatattag cccttggttt ggtgtgcaat aaagtttggc aaacaaaaag 1980
2197 gtttaatcct gctaatacaa gtatcacaaa ttatgaaatc aagcatgaac ctgctgcgtt 2040
2198 tgatctgaga ggaggacctc gctcggcaga acacgtcgat atacttggac attcagagct 2100
2199 aaatgtatgt tcattttacc ttacaaattt ctattactaa ctcttgaaat aaggaaatta 2160
2200 ttttaaaagt ttcatcaggc catggtgact cggtaccaaa ccgttatata tcagatatcc 2220
2201 agtacggaca taagtttgt agattgcaat taactaacta accgaacagg gaaataataa 2280
2202 atgagataaa tctcgataaa cctagaaatt aa                             2312
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E--> 2205 <210> SEQ ID NO: (4b)24
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     2207 <212> TYPE: DNA
     2208 <213> ORGANISM: Arabidopsis thaliana
     2210 <400> SEQUENCE: (4b)24
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2213 gtggtgcacg atgaggattc gcaaaagaaa ccacacgaat cttccaaatc ccaccataag 120
2214 aaatcgaacg gaggagggaa gtggtcgtgc atcgattctt gttgttggtt cattgggtgt 180
2215 gtgtgtgtaa cctggtggtt tcttctcttc ctttacaacg caatgcctgc gagcttccct 240
2216 cagtatgtaa cggagcgaat cacgggtcct ttgcctgacc cgcccggtgt taagctcaaa 300
2217 aaagaaggtc ttaaggcgaa acatcctgtt gtcttcattc ctgggattgt caccggtggg 360
2218 ctcgagcttt gggaaggcaa acaatgcgct gatggtttat ttagaaacg tttgtggggt 420
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2224 gtcatcttat tgccaaatct gttgctagac atgccctaga gtccgttcat aacaagttac 780
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2226 tatgttttgt tgggaataga gaagttctaa ctacatctgt ggaaagtgtg ttcaggctgt 900
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2237 ttctcatcgt tctttctatt attctgttcc atgttacgtt tctttcttca ttacttaagg 1560
2238 cttaaatatg tttcatgttg aattaatagg tacgtgatca gactcttagc cgtatgaaaa 1620
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RAW SEQUENCE LISTING   DATE: 06/25/2002
PATENT APPLICATION: US/09/537,710A TIME: 10:02:45

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\06252002\I537710A.raw

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2283 <222> LOCATION: (120)..(401)
2285 <221> NAME/KEY: Unsure
2286 <222> LOCATION: 1..401
2287 <223> OTHER INFORMATION: n is c, g, a, t or u.
2289 <221> Unsure
2290 <222> LOCATION: 1..401
2291 <223> OTHER INFORMATION: Xaa = unknown
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2297 ctggacgaga tttgacaaag tccgtatagc ttaacctggt ttaatttcaa gtgacagat  119
2299 atg ccc ctt att cat cgg aaa aag ccg acg gag aaa cca tcg acg ccg  167
2300 Met Pro Leu Ile His Arg Lys Lys Pro Thr Glu Lys Pro Ser Thr Pro
2301  1               5                   10                  15
2303 cca tct gaa gag gtg gtg cac gat gag gat tcg caa aag aaa cca cac  215
2304 Pro Ser Glu Glu Val Val His Asp Glu Asp Ser Gln Lys Lys Pro His
2305             20                  25                  30
2307 gaa tct tcc aaa tcc cac cat aag naa tcg aac gga gga ggg aag tgg  263
2308 Glu Ser Ser Lys Ser His His Lys Xaa Ser Asn Gly Gly Gly Lys Trp
2309         35                  40                  45
2311 tcg tgc atc gat tct tgt tgt tgg ttc att ggg tgt gtg tgt gta acc  311
2312 Ser Cys Ile Asp Ser Cys Cys Trp Phe Ile Gly Cys Val Cys Val Thr
2313         50                  55                  60
2315 tgg tgg ttt ctt ctc ttc ctt tac aac gca atg cct gcg agc ttc cct  359
2316 Trp Trp Phe Leu Leu Phe Leu Tyr Asn Ala Met Pro Ala Ser Phe Pro
2317 65                  70                  75                  80
2319 cag tat gta acg gag ccg aat cac gng tcc ttt gcc tta ccc g        402
2320 Gln Tyr Val Thr Glu Pro Asn His Xaa Ser Phe Ala Leu Pro
2321             85                  90
2326 <210> SEQ ID NO: 6b 26
2327 <211> LENGTH: 643
2328 <212> TYPE: DNA
2329 <213> ORGANISM: Zea mays
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2332 <221> NAME/KEY: CDS
2333 <222> LOCATION: (1)..(402)
2335 <400> SEQUENCE: 6b 26
2337 cgg gag aaa ata gct gct ttg aag ggg ggt gtt tac tta gcc gat ggt  48
2338 Arg Glu Lys Ile Ala Ala Leu Lys Gly Gly Val Tyr Leu Ala Asp Gly
2339  1               5                   10                  15
2341 gat gaa act gtt cca gtt ctt agt gcg ggc tac atg tgt gcg aaa gga  96
2342 Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly
2343             20                  25                  30
2345 tgg cgt ggc aaa act cgt ttc agc cct gcc ggc agc aag act tac gtg  144
2346 Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val
2347         35                  40                  45
2349 aga gaa tac agc cat tcg cca ccc tct act ctc ctg gaa ggc agg ggc  192
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see p. 18 for more error

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2350 Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly
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2353 acc cag agc ggt gca cat gtt gat ata atg ggg aac ttt gct cta att   240
2354 Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
2355     65                  70                  75                  80
2357 gag gac gtc atc aga ata gct gct ggg gca acc ggt gag gaa att ggt   288
2358 Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly
2359                     85                  90                  95
2361 ggc gat cag gtt tat tca gat ata ttc aag tgg tca gag aaa atc aaa   336
2362 Gly Asp Gln Val Tyr Ser Asp Ile Phe Lys Trp Ser Glu Lys Ile Lys
2363                    100                 105                 110
2365 ttg aaa ttg taa cct atg gga agt taa aga agt gcc gac ccg ttt att   384
2366 Leu Lys Leu     Pro Met Gly Ser     Arg Ser Ala Asp Pro Phe Ile
2367         115                 120                 125
2369 gcg ttc caa agt gtc ctg cctgagtgca actctggatt ttgcttaaat         432
2370 Ala Phe Gln Ser Val Leu
2371         130
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2377 tgcatttgcc agctgaaatt gtgtagtcgt tttctttacg atttaatanc aagtggcgga 612
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2383 <211> LENGTH: 115
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2392             20                  25                  30
2393 Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val
2394         35                  40                  45
2395 Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly
2396     50                  55                  60
2397 Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
2398 65                  70                  75                  80
2399 Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly
2400                     85                  90                  95
2401 Gly Asp Gln Val Tyr Ser Asp Ile Phe Lys Trp Ser Glu Lys Ile Lys
2402                    100                 105                 110
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2409 <211> LENGTH: 516
2410 <212> TYPE: DNA
2411 <213> ORGANISM: Neurospora crassa
2413 <220> FEATURE:
2414 <221> NAME/KEY: Unsure
2415 <222> LOCATION: 1..516
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     2422 ggaagccgac ggagcgagcc tacatctatc tggcgcccga tcccgggacg acaacgcatc 180
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     2424 gcgaaggcga tggcacagtg aaccttatga gtttggggta cctgtgcaat aaggggtgga 300
     2425 aaatgaagag atacaatcct gcgggctcaa aaataaccgt ggtcgagatg ccgcatgaac 360
     2426 cagaacggtt caatccgaga ggagggccga atacggcgga cttaaatatg tagaaaaggt 420
     2427 tgaaatttat gaagagtaat taaatacggc acataggtta ctcaatagta tgactaatta 480
     2428 aaaaaaaatt ttttttctaa aaaaaaaaaa aaaaaa 516
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     2433 <211> LENGTH: 1562
     2434 <212> TYPE: DNA
     2435 <213> ORGANISM: Arabidopsis thaliana
     2437 <400> SEQUENCE: (9b) 29
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     2441 ggaggtaacc agctagaggt acggctggac agagaataca agccaagtag tgtctggtgt 180
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see item 9

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     2547 <400> SEQUENCE: (11b) 31

```
2549 ctggggccaa aagtgaacat aacaaggaca ccacagtcag agcatgatgt tcagatgtac 60
2550 aagtgcatct aaatatagag catcaacatg gtgaagatat cattcccaat atgacaaagt 120
2551 tacctacaat gaagtacata acctattatg aggattctga aagttttcca gggacaagaa 180
2552 cagcagtttg ggagcttgat aaagcaaatc acaggaacat tgtcagatct ccagctttga 240
2553 tgcgggagct gtggcttgag atgtggcatg atattcatcc tgataaaaag tccaagtttg 300
2554 ttacaaaagg tggtgtctga tcctcactat tttcttctat aaatgtttga gtttgtattg 360
2555 acattgtaag tattgcaaca aaaagcaaag cgtgggcctc tgagggatga ggactgctat 420
2556 tgggattacg ggaaagctcg atgtgcatgg gctgaacatt gtgaatacag gttagaatat 480
2557 tcaaattata ttttgcaaaa tattctcttt ttgtgtattt aggccacctt tccccggtca 540
2558 caacgatgca gatatgtatt cggggatgtt cacctgggac agagttgcag attgaagagt 600
2559 tctacatctc acatcctgtc acactatgtg tgatatttaa gaaactttgt ttggcggaac 660
2560 aacaagtttg cacaaacatt tgaagaagaa agcgaaatga ttcagagag      709
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 06/25/2002
PATENT APPLICATION: US/09/537,710A   TIME: 10:02:46

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\06252002\I537710A.raw

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 9

VERIFICATION SUMMARY   DATE: 06/25/2002
PATENT APPLICATION: US/09/537,710A   TIME: 10:02:46

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\06252002\I537710A.raw

```
L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:2340
L:662 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:694 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:698 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:704 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:552
L:706 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:612
L:754 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:755 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:60
L:757 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:180
L:1228 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 1a
L:1362 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 2a
L:1445 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 3a
L:1528 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 4a
L:1708 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 5a
L:1841 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 1b
L:2021 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 2b
L:2157 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 3b
L:2205 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 4b
L:2276 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 5b
L:2289 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:2293 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:2307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:215
L:2308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:263
L:2319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:359
L:2320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:402
L:2326 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 6b
L:2367 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:2371 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:2377 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:2377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:552
L:2379 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:2379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:612
L:2382 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 7b
L:2408 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 8b
L:2420 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:2421 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:60
L:2423 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:180
L:2432 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 9b
L:2468 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 10b
L:2542 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO: 11b
```